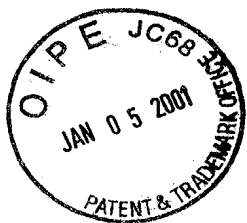


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 65 70 75 80

Gly Ala Ile Asn Val Thr Tyr Arg Tyr Leu Ala Ala Thr Pro Leu Gln  
 85 90 95

Arg Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys  
 100 105 110

Gly Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser

115

120

125

Tyr Glu Glu Leu Lys Glu Ile Ser Val Val Ile His Leu Ala Asp Phe  
 130 135 140

Asn Ser Ser Trp Arg Asp Ala Met Val Gln Asp Ile Thr Gln Lys Phe  
 145 150 155 160

Ala His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu  
 165 170 175

Glu Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro  
 180 185 190

Glu Asp Arg Val Lys Phe Arg Ser Lys Gln Asn Val Asp Tyr Thr Phe  
 195 200 205

Leu Leu Asn Phe Cys Ala Asn Thr Ser Asp Tyr Tyr Val Met Leu Glu  
 210 215 220

Asp Asp Val Arg Cys Ser Lys Asn Phe Leu Thr Ala Ile Lys Lys Val  
 225 230 235 240

Ile Ala Ser Leu Glu Gly Thr Tyr Trp Val Thr Leu Glu Phe Ser Lys  
 245 250 255

Leu Gly Tyr Ile Gly Lys Leu Tyr His Ser His Asp Leu Pro Arg Leu  
 260 265 270

Ala His Phe Leu Leu Met Phe Tyr Gln Glu Met Pro Cys Asp Trp Leu  
 275 280 285

Leu Thr His Phe Arg Gly Leu Leu Ala Gln Lys Asn Val Ile Arg Phe  
 290 295 300

Lys Pro Ser Leu Phe Gln His Met Gly Tyr Tyr Ser Ser Tyr Lys Gly  
 305 310 315 320

Thr Glu Asn Lys Leu Lys Asp Asp Asp Phe Glu Glu Glu Ser Phe Asp  
 325 330 335

Ile Pro Asp Asn Pro Pro Ala Ser Leu Tyr Thr Asn Met Asn Val Phe  
 340 345 350

Glu Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe  
 355 360 365

Trp Gly Lys Pro Pro Ser Thr Gly Asp Val Phe Val Ile Val Phe Glu  
 370 375 380

Asn Pro Ile Ile Ile Lys Lys Ile Lys Val Asn Thr Gly Thr Glu Asp  
 385 390 395 400

Arg Gln Asn Asp Ile Leu His His Gly Ala Leu Asp Val Gly Glu Asn  
 405 410 415

Val Met Pro Ser Lys Gln Arg Gly Gln Cys Ser Thr Tyr Leu Arg Leu  
 420 425 430

Gly Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys  
 435 440 445

Ile Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln  
 450 455 460

Lys Glu Trp Leu Ile Ile Arg Ser Ile Ser Ile Trp Thr Ser  
 465 470 475

<210> 9  
 <211> 1005  
 <212> DNA  
 <213> Homo sapiens

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 ctcattggcg tgctgcccatt cttcttcggc gccctgcgct ccgtacgctg cgcccgcggc 180  
 aagaatgctt cagacatgcc tgaacaacat accagccggg atgccgcccg cttccccatc 240  
 atcgccagct gcacactctt ggggctctac ctctttttca aaatattctc ccaggagtac 300  
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 atcagcccct tcatgaataa gttttttcca gccagctttc caaatcgaca gtaccagctg 420

ctcttcacac aggggttctgg ggaaaacaag gaagagatca tcaattatga atttgacacc 480  
aaggacctgg tgtgcctggg cctgagcagc atcgttggcg tctggtacct gctgaggaag 540  
gtatttggca ccaatgtgat ggtgacagtg gccaaagtcct tcgaggcacc aataaaattg 600  
gtgtttcccc aggatctgct ggagaaaggc ctggaagcaa acaactttgc catgctggga 660  
cttgagatg tcgtcattcc agggatcttc attgccttgc tgctgcgctt tgacatcagc 720  
ttgaagaaga ataccacac ctacttctac accagctttg cagcctacat cttcggcctg 780  
ggccttacca tcttcatcat gcacatcttc aagcatgctc agcctgcctt cctatacctg 840  
gtccccgcct gcacgggttt tctgtctctg gtggcgctgg ccaagggaga agtgacagag 900  
atgttcagtt atgaggagtc aaatcctaag gatccagcgg cagtgcagaga atccaaagag 960  
ggaacagagg catcagcatc gaaggggctg gagaagaaag agaaa 1005

<210> 10  
<211> 1486  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Clone OA004b derived from T98G cell

<220>  
<221> CDS  
<222> (117)..(1121)

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ctgcgtccct gctgcagcaa ccggagctgg agtcggatcc cgaacgcacc ctgcgc atg 119  
Met  
1

gac tcg gcc ctc agc gat ccg cat aac ggc agt gcc gag gca ggc ggc 167  
Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly  
5 10 15

ccc acc aac agc act acg cgg ccg cct tcc acg ccc gag ggc atc gcg 215  
Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala  
20 25 30

ctg gcc tac ggc agc ctc ctg ctc atg gcg ctg ctg ccc atc ttc ttc 263  
Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe  
35 40 45

ggc gcc ctg cgc tcc gta cgc tgc gcc cgc ggc aag aat gct tca gac Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp 50 55 60 65	311
atg cct gaa aca atc acc agc cgg gat gcc gcc cgc ttc ccc atc atc Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile 70 75 80	359
gcc agc tgc aca ctc ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser 85 90 95	407
cag gag tac atc aac ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly 100 105 110	455
atc ctg gcc ctg tcc cac acc atc agc ccc ttc atg aat aag ttt ttt Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe 115 120 125	503
cca gcc agc ttt cca aat cga cag tac cag ctg ctc ttc aca cag ggt Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly 130 135 140 145	551
tct ggg gaa aac aag gaa gag atc atc aat tat gaa ttt gac acc aag Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys 150 155 160	599
gac ctg gtg tgc ctg ggc ctg agc agc atc gtt ggc gtc tgg tac ctg Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu 165 170 175	647
ctg agg aag gta ttt ggc acc aat gtg atg gtg aca gtg gcc aag tcc Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys Ser 180 185 190	695
ttc gag gca cca ata aaa ttg gtg ttt ccc cag gat ctg ctg gag aaa Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys 195 200 205	743
ggc ctc gaa gca aac aac ttt gcc atg ctg gga ctt gga gat gtc gtc Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val 210 215 220 225	791
att cca ggg atc ttc att gcc ttg ctg ctg cgc ttt gac atc agc ttg Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu 230 235 240	839
aag aag aat acc cac acc tac ttc tac acc agc ttt gca gcc tac atc Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile 245 250 255	887
ttc ggc ctg ggc ctt acc atc ttc atc atg cac atc ttc aag cat gct Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His Ala 260 265 270	935



cag cct gcc ctc cta tac ctg gtc ccc gcc tgc atc ggt ttt cct gtc 983  
 Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val  
 275 280 285

ctg gtg gcg ctg gcc aag gga gaa gtg aca gag atg ttc agt tat gag 1031  
 Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu  
 290 295 300 305

gag tca aat cct aag gat cca gcg gca gtg aca gaa tcc aaa gag gga 1079  
 Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly  
 310 315 320

aca gag gca tca gca tcg aag ggg ctg gag aag aaa gag aaa 1121  
 Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys  
 325 330 335

tgatgcggct ggtgcccgag cctctcaggg ccagaccaga cagatggggg ctgggcccac 1181

acaggcgtgc accggtagag ggcacaggag gccaaaggga gctccaggac agggcagggg 1241

gcagcaggat acctccagcc aggcctctgt ggccctctgtt tccttctccc tttcttgccc 1301

ctcctctgct cctccccaca cctgcaggc aaaagaaacc ccagcttcc cccctccccg 1361

ggagccaggt gggaaaagtg ggtgtgattt ttagattttg tattgtggac tgattttgcc 1421

tcacattaaa aactcatccc atggccaggg cgggccactg tgctcctgaa aaaaaaaaaa 1481

aaaaa 1486

<210> 11  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Clone OA004b derived from T98G cell

<400> 11

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly  
 1 5 10 15

Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile  
 20 25 30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe  
 35 40 45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser  
 50 55 60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile  
 65 70 75 80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe  
 85 90 95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu  
 100 105 110

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe  
 115 120 125

Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln  
 130 135 140

Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr  
 145 150 155 160

Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr  
 165 170 175

Leu Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys  
 180 185 190

Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu  
 195 200 205

Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val  
 210 215 220

Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser  
 225 230 235 240

Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr  
 245 250 255

Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His  
 260 265 270

Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro  
 275 280 285

Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr  
 290 295 300

Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu  
 305 310 315 320

Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys  
 325 330 335

<210> 12  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 12  
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 agtcaactag tgaattcaaa caacttgaag ctcaatttct ggaaatctcc ctccctccttc 180  
 aatcggcctg tggatgtcct ggtcccatct gtcagtctgc aggcatttaa atccttctctg 240  
 agatcccagg gcttagagta cgcagtgaca attgaggacc tgcaggccct tttagacaat 300  
 gaagatgatg aaatgcaaca caatgaaggg caagaacgga gcagtaataa cttcaactac 360  
 ggggcttacc attccctgga agctatttac cacgagatgg acaacattgc cgcagacttt 420  
 cctgacctgg cgaggagggg gaagattgga cattcggttg aaaaccggcc gatgtatgta 480  
 ctgaagttca gcactgggaa aggcgtgagg cggccggccg tttggctgaa tgcaggcatc 540  
 cattcccgag agtggatctc ccaggccact gcaatctgga cggcaaggaa gattgtatct 600  
 gattaccaga gggatccagc tatcacctcc atcttgagaa aaatggatat tttcttggtg 660  
 cctgtggcca atcctgatgg atatgtgtat actcaaactc aaaaccgatt atggaggaag 720  
 acgcgggtccc gaaatcctgg aagctcctgc attggtgctg acccaaatag aagctggaac 780  
 gctagttttg caggaaaggg agccagcgac aacccttgct ccgaagtgta ccatggaccc 840  
 cacgccaat cggaagtgga ggtgaaatca gtggtagatt tcatccaaaa acatgggaat 900  
 ttcaagtgtc tcatcgacct gcacagctac tcgcagctgc tgatgtatcc atatgggtac 960

tcagtcaaaa aggccccaga tgccgaggaa ctgcacaagg tggcgaggct tgcggccaaa 1020  
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<210> 13  
<211> 3156  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> Clone OAF075b derived from human bone marrow stroma cell HAS303

<220>  
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<220>  
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<222> (11)..(58)

<220>  
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<222> (59)..()

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Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser  
-15 -10 -5  
  
agc atc tgt ggc caa gaa aaa ttt ttt ggg gac caa gtt ttt agg att 97  
Ser Ile Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile  
-1 1 5 10  
  
aat gtc aga aat gga gac gag atc agc aaa ttg agt caa cta gtg aat 145  
Asn Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn  
15 20 25  
  
tca aac aac ttg aag ctg aat ttc tgg aaa tct ccc tcc tcc ttc aat 193  
Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn  
30 35 40 45  
  
cgg cct gtg gat gtc ctg gtc cca tct gtc agt ctg cag gca ttt aaa 241  
Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys  
50 55 60  
  
tcc ttc ctg aga tcc cag ggc tta gag tac gca gtg aca att gag gac 289  
Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp  
65 70 75  
  
ctg cag gcc ctt tta gac aat gaa gat gat gaa atg caa cac aat gaa 337  
Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu  
80 85 90

ggg caa gaa cgg agc agt aat aac ttc aac tac ggg gct tac cat tcc	385
Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser	
95 100 105	
ctg gaa gct att tac cac gag atg gac aac att gcc gca gac ttt cct	433
Leu Glu Ala Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro	
110 115 120 125	
gac ctg gcg agg agg gtg aag att gga cat tcg ttt gaa aac cgg ccg	481
Asp Leu Ala Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro	
130 135 140	
atg tat gta ctg aag ttc agc act ggg aaa ggc gtg agg cgg ccg gcc	529
Met Tyr Val Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala	
145 150 155	
gtt tgg ctg aat gca ggc atc cat tcc cga gag tgg atc tcc cag gcc	577
Val Trp Leu Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala	
160 165 170	
act gca atc tgg acg gca agg aag att gta tct gat tac cag agg gat	625
Thr Ala Ile Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp	
175 180 185	
cca gct atc acc tcc atc ttg gag aaa atg gat att ttc ttg ttg cct	673
Pro Ala Ile Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro	
190 195 200 205	
gtg gcc aat cct gat gga tat gtg tat act caa act caa aac cga tta	721
Val Ala Asn Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu	
210 215 220	
tgg agg aag acg cgg tcc cga aat cct gga agc tcc tgc att ggt gct	769
Trp Arg Lys Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala	
225 230 235	
gac cca aat aga agc tgg aac gct agt ttt gca gga aag gga gcc agc	817
Asp Pro Asn Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser	
240 245 250	
gac aac cct tgc tcc gaa gtg tac cat gga ccc cac gcc aat tcg gaa	865
Asp Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu	
255 260 265	
gtg gag gtg aaa tca gtg gta gat ttc atc caa aaa cat ggg aat ttc	913
Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe	
270 275 280 285	
aag tgc ttc atc gac ctg cac agc tac tcg cag ctg ctg atg tat cca	961
Lys Cys Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro	
290 295 300	
tat ggg tac tca gtc aaa aag gcc cca gat gcc gag gaa ctc gac aag	1009
Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys	

305

310

315

gtg gcg agg ctt gcg gcc aaa gct ctg gct tct	gtg tcg ggc act gag	1057
Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser	Val Ser Gly Thr Glu	
320	325 330	
tac caa gtg ggt ccc acc tgc acc act gtc tta	taaactgccca aaactgggag	1110
Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Leu		
335	340	
atactcatca gattgctcca acagaagagg aggaaggctc	tcccgagggc tgtccaggag	1170
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cagcctctag caaccctttc cctcctctct cactgattct	gctccaggaa gggcttggaa	2010
acaagttctt tgggttcctc tgacttgtgg ataacacagt	ttcatgtact ttttgtagtt	2070
cataagcgtg gtgattgggt tttcacgctc atgtgtgaca	tatgccttcc tccaattttg	2130
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tatccatagt tacaaaagac atgtacaggg gccaaaggaa	aacttccctt ttgccttctg	2250
aaggttcatt gaaaaatcaa ctgaccaaag gcagatcgat	aggagaaaag gcatacaaaa	2310
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tggggcacag aagcttgtat accctttttc atacaggagg	gaggagatgt atggactggg	2430
gagggtgggag gcagatatta caggaagggtg aggggaggag	ctgtacagga acaaagcttg	2490

tcttattaag cagataaagt cctccaggca atctcttgga gctgctctca gaagaataga 2550  
tgaagtctgt ctgggtgtgg tgatgattcc cagtctcacc tcttctggtg gtttatcttt 2610  
cttggttatt tgatgagacc tctagggagg gtgtttaaga caattgcatt tcttttggaa 2670  
agatgctttc ttggtcagat gaggaaattt ccaaagacag acagtccttc cctgtgtttg 2730  
gtggtggggc aggtatgggg aacaagaagt tagagggacc ttggttcggg ggcggcttct 2790  
gagggccttc agcatgtcaa aacatcagcc tttgggatat cactttctga gcccacaacc 2850  
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acacaatgca gcactacgga gcccttaa atgaatgaggta gatctatgtg cgctaaaagg 2970  
gaatactcac caattgttaa ttgaaaaata catgtgcaga acagcgtaa tagtgtgttc 3030  
ccattttttg ttgttggtat tgtttttaaa gagtaggtag actttcagca gggacccaaa 3090  
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aaaaaa 3156

<210> 14  
<211> 360  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Clone OAF075b derived from human bone marrow stroma cell HAS303  
<400> 14

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Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile Asn Val Arg  
1 5 10 15

Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn Ser Asn Asn  
20 25 30

Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn Arg Pro Val  
35 40 45

Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys Ser Phe Leu  
50 55 60

Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp Leu Gln Ala  
65 70 75 80

Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu Gly Gln Glu  
85 90 95

Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser Leu Glu Ala  
100 105 110

Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro Asp Leu Ala  
115 120 125

Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro Met Tyr Val  
130 135 140

Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu  
145 150 155 160

Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile  
165 170 175

Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile  
180 185 190

Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn  
195 200 205

Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys  
210 215 220

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro Asn  
225 230 235 240

Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp Asn Pro  
245 250 255

Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu Val Glu Val  
260 265 270

Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe Lys Cys Phe



275

280

285

Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr  
290 295 300

Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys Val Ala Arg  
305 310 315 320

Leu Ala Ala Lys Ala Leu Ala Ser Val Ser Gly Thr Glu Tyr Gln Val  
325 330 335

Gly Pro Thr Cys Thr Thr Val Leu  
340

<210> 15  
<211> 35  
<212> DNA  
<213> Artificial

<220>  
<223> Primer

<220>  
<221> misc\_feature  
<223> n can be any nucleotide

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35

<210> 16  
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<212> DNA  
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